

Fig. 1

1B

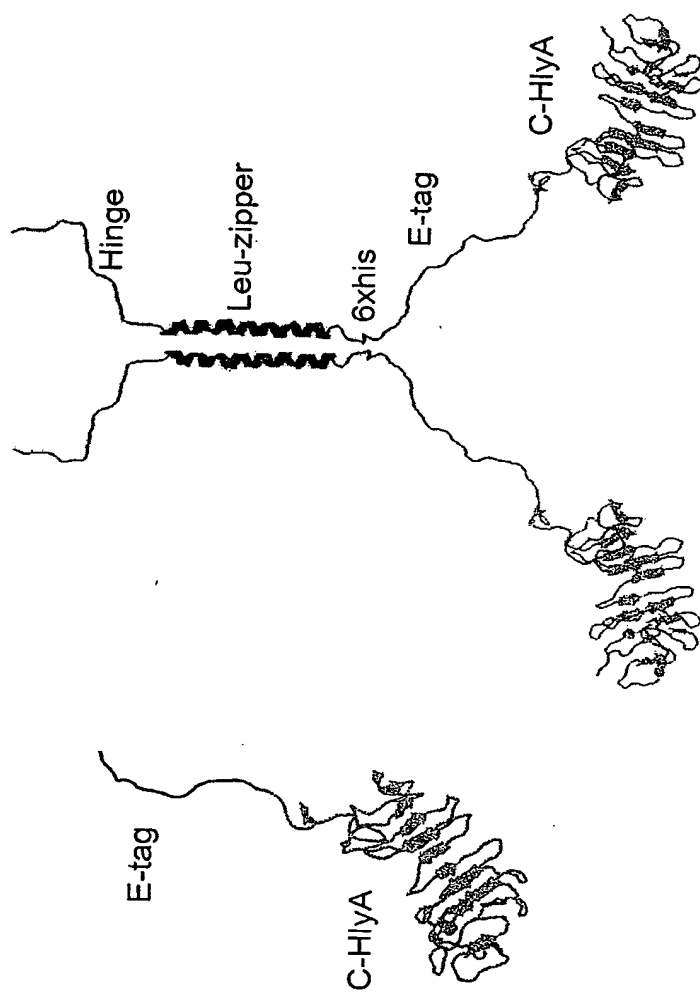


Fig. 1 (cont.)

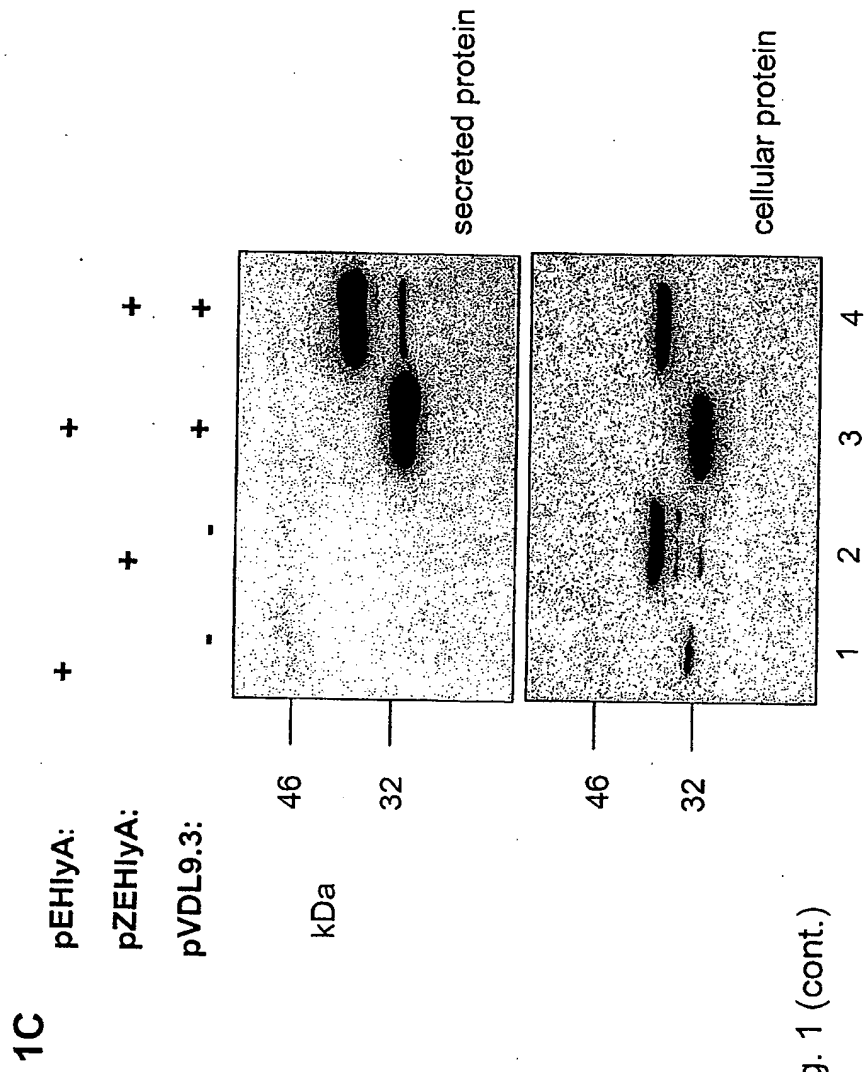


Fig. 1 (cont.)

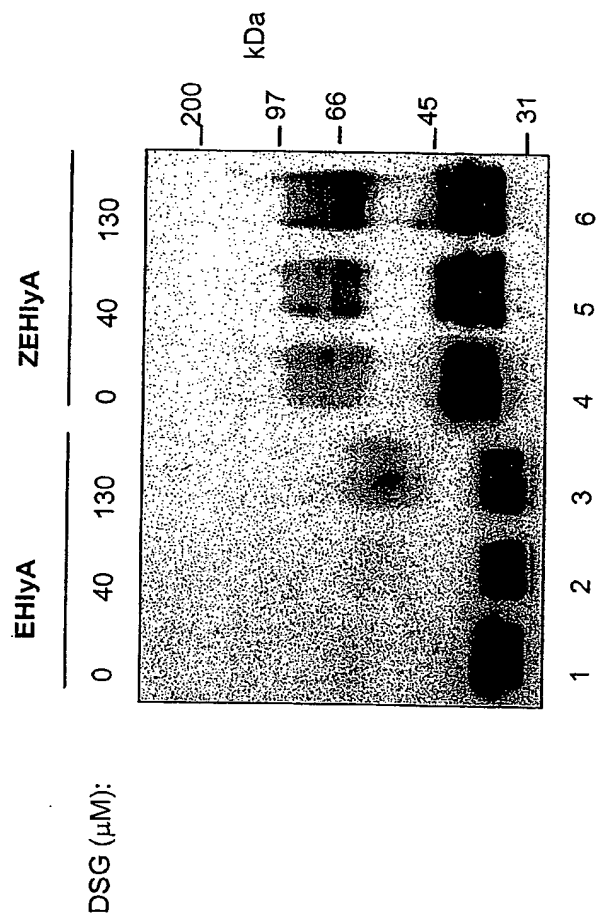


Fig. 2

3A

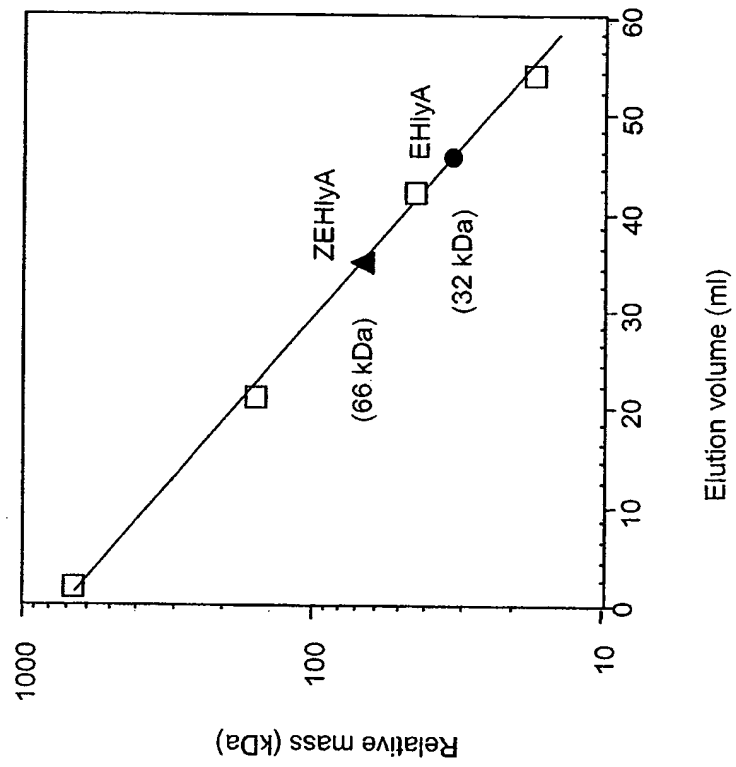
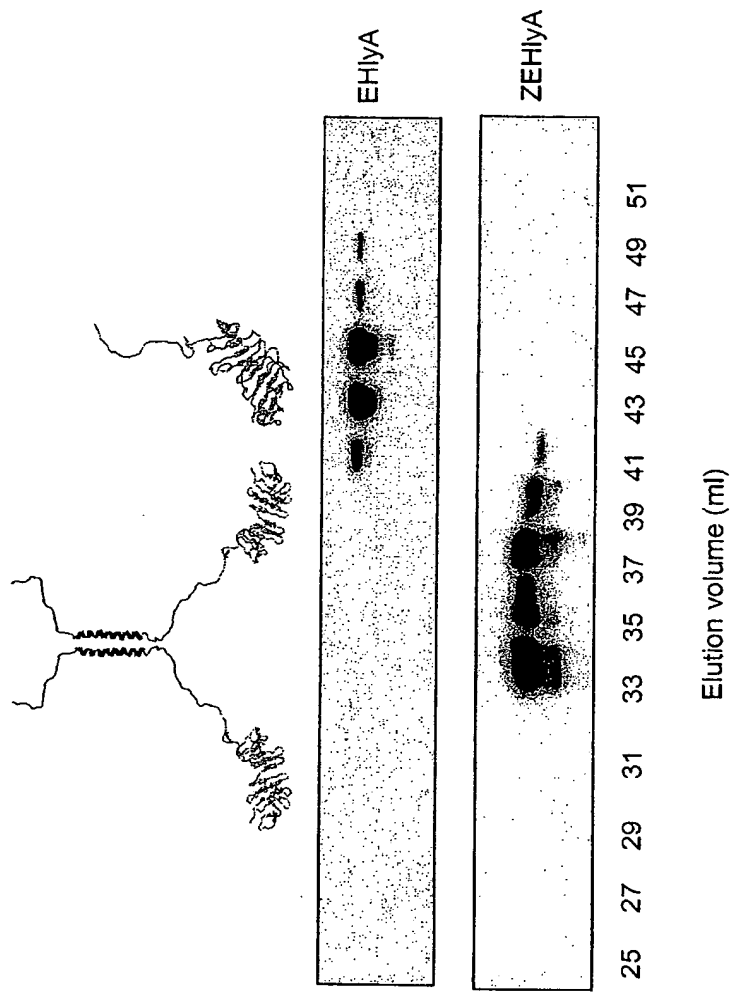


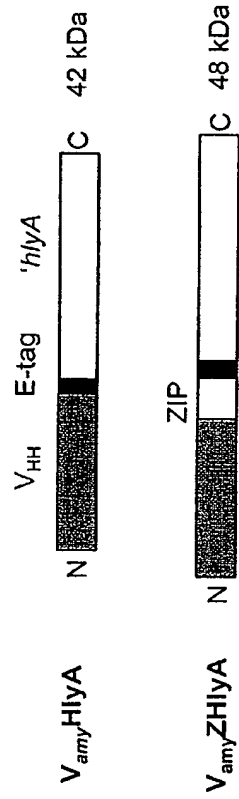
Fig. 3

3B

Fig. 3 (cont.)



4A



4B

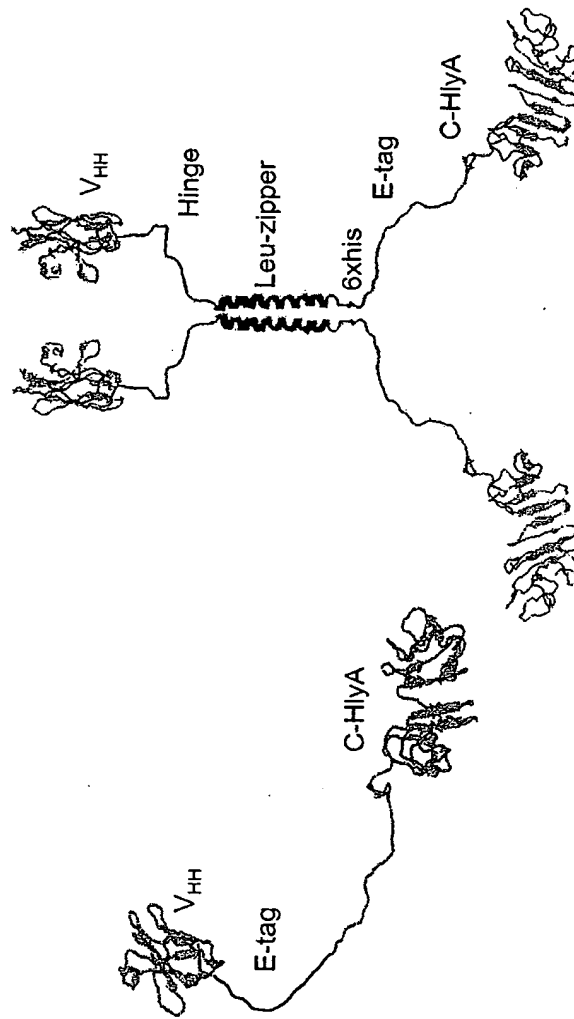


Fig. 4

4C

4D

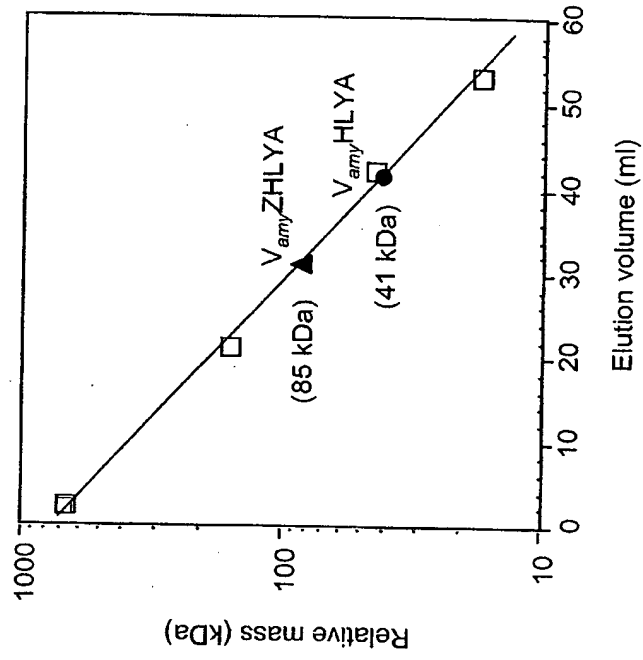
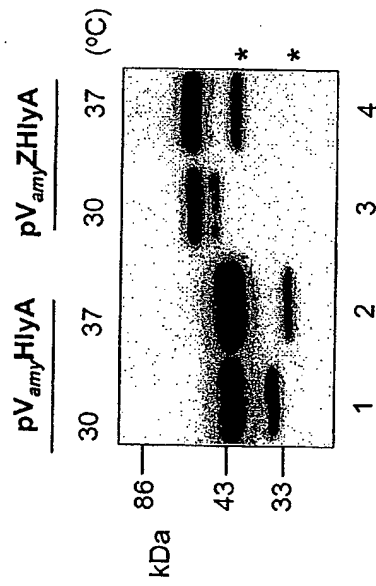
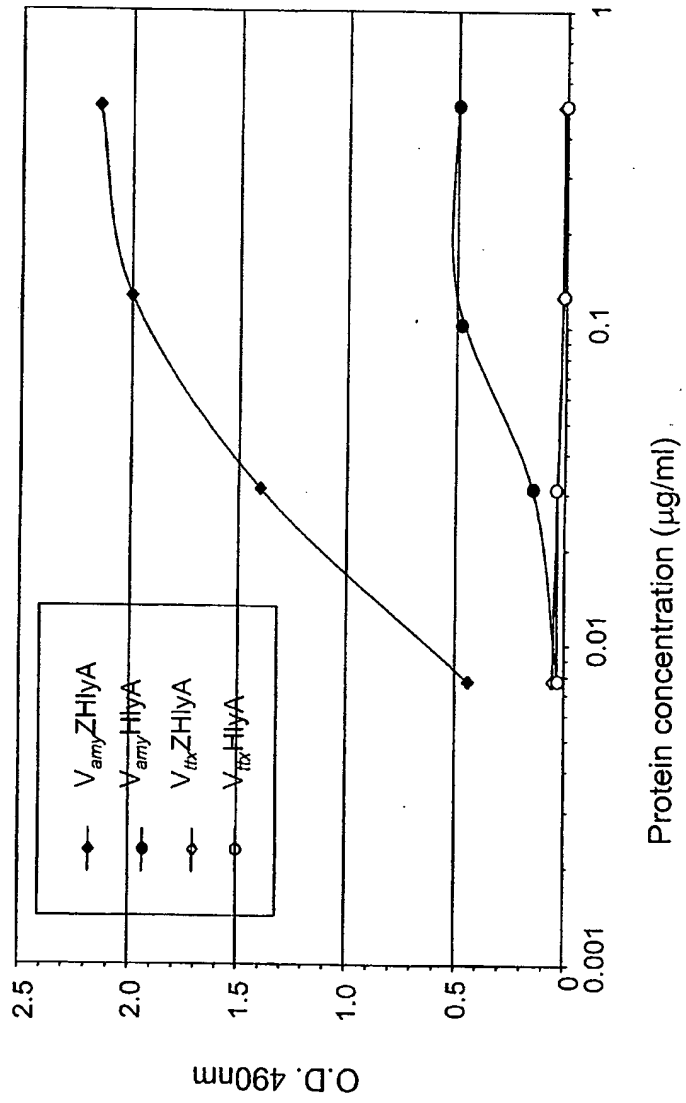


Fig. 4 (cont.)



Fig. 5



pZEHlyA map

AGCGGATAACAATTCACACAGGAAACAGCT (sequence before the ATG)

Fig. 6

```

GGTAATGACAAGTTGTACGGCAGTGAGGGAGCAGACCTGCTTGATGGCGGAGAAGGGAAT
301 -----+-----+-----+-----+-----+ 360
CCATTACTGTTCAACATGCCGTCACCTCCCTCGTCTGGACGAACTACCGCCTCTTCCCTTA

a   G N D K L Y G S E G A D L L D G G E G N -

GATCTTCTGAAAGGTGGATATGGTAATGATATTTATCGTTATCTTTCAGGATATGGCCAT
361 -----+-----+-----+-----+-----+ 420
CTAGAAGACTTTCCACCTATACCATTACTATAAATAGCAATAGAAAGTCCTATACCGGTA

a   D L L K G G Y G N D I Y R Y L S G Y G H -

CATATTATTGACGATGAAGGGGGAAAGACGATAAACTCAGTTTAGCTGATATAGATTTTC
421 -----+-----+-----+-----+-----+ 480
GTATAATAACTGCTACTTCCCCCTTTCTGCTATTTGAGTCAAATCGACTATATCTAAAG

a   H I I D D E G G K D D K L S L A D I D F -

CGGGACGTTGCCTTTAAGCGAGAAGGGAATGACCTCATTATGTATAAAGCTGAAGGTAAT
481 -----+-----+-----+-----+-----+ 540
GCCCTGCAACGGAAATTCGCTCTTCCCTTACTGGAGTAATACATATTTGACTTCCATTA

a   R D V A F K R E G N D L I M Y K A E G N -

GTTCTTTCTATTGGCCACAAAAATGGTATTACATTTAAAACTGGTTTGAAAAGAGTCA
541 -----+-----+-----+-----+-----+ 600
CAAGAAAGATAACCGGTGTTTTTACCATAATGTAAATTTTGACCAAACCTTTTCTCAGT

a   V L S I G H K N G I T F K N W F E K E S -

GATGATCTCTCTAATCATCAGATAGAGCAGATTTTTGATAAAGACGGCAGGGTAATCACA
601 -----+-----+-----+-----+-----+ 660
CTACTAGAGAGATTAGTAGTCTATCTCGTCTAAAACTATTTCTGCCGTCCCATTAGTGT

a   D D L S N H Q I E Q I F D K D G R V I T -

CCAGATTCTCTTAAAAAAGCATTTTGAATATCAGCAGAGTAATAACAAGGTAAGTTATGTG
661 -----+-----+-----+-----+-----+ 720
GGTCTAAGAGAATTTTTTCGTAAACTTATAGTCGTCTCATTATTGTTCCATTCAATACAC

a   P D S L K K A F E Y Q Q S N N K V S Y V -

TATGGACATGATGCATCAACTTATGGGAGCCAGGACAATCTTAATCCATTAATTAATGAA
721 -----+-----+-----+-----+-----+ 780
ATACCTGTACTACGTAGTTGAATACCCTCGGTCCTGTTAGAATTAGGTAATTAATTACTT

a   Y G H D A S T Y G S Q D N L N P L I N E -

```

Fig. 6 (cont.)

PstI  
|

781 ATCAGCAAAATCATTTCAGCTGCAGGTAACCTCGATGTTAAGGAGGAAAGATCTGCCGCT  
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 840  
TAGTCGTTTTAGTAAAGTCGACGTCCATTGAAGCTACAATTCCTCCTTTCTAGACGGCGA

a I S K I I S A A G N F D V K E E R S A A -

NdeI  
|

841 TCTTTATTGCAGTTGTCCGGTAATGCCAGTGATTTTTCATATGGACGGAACCTCAATAACT  
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 900  
AGAAATAACGTCAACAGGCCATTACGGTCACTAAAAAGTATACCTGCCTTGAGTTATTGA

a S L L Q L S G N A S D F S Y G R N S I T -

TTGACAGCATCAGCATAA

901 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 918  
AACTGTCGTAGTCGTATT

a L T A S A \* -

Cutting enzymes:

AccI	BamHI	EcoRI	HindIII	NdeI	PstI	SacI	SalI
SmaI	XbaI						

Not cutting enzymes:

KpnI	NcoI	NheI	NotI	SacII	SphI
------	------	------	------	-------	------

Fig. 6 (cont.)

BglII EcoRI

Xba I

NcoI

NheI

Sfil

SalI

b M A S T A S G A A S T S G G P K P S T P -  
|=> Ig hinge

XmaI

```

b      P G S S R M K Q L E D K V E E L L S K N -
      |=> Leu-zipper GCN4

```

XbaI

HindIII

b Y H L E N E V A R L K K L V G E R G G H -

SalI

XmaI

BamHI

301 CCATCACCATCACCATGCGTCGACGCCCGGGGGTGC CGCGGTGCCGTATCCGGATCCGCT  
-----+-----+-----+-----+-----+-----+-----+ 360  
GGTAGTGGTAGTGGTACGCAGCTGCGGGCCCCACGCGGCCACGGCATAGGCCTAGGCCGA

Fig. 7

b        H H H H H A S T P G G A P V P Y P D P L -  
           6xhis tag                    | => E-tag  
           EagI  
           |  
 361 -----+-----+-----+-----+-----+ 420  
       GGAACCGGCCGGGGAAAATTCTCTTGCTAAAAATGTATTATCCGGTGGAAAAGGTAATGA  
       CCTTGGCCGGCCCTTTTAAGAGAACGATTTTACATAATAGGCCACCTTTTCCATTACT

b        E P A G E N S L A K N V L S G G K G N D -  
           | => C-hlyA  
 421 -----+-----+-----+-----+-----+ 480  
       CAAGTTGTACGGCAGTGAGGGAGCAGACCTGCTTGATGGCGGAGAAGGAATGATCTTCT  
       GTTCAACATGCCGTCACCTCCCTCGTCTGGACGAACCTACGCCTCTTCCCTTACTAGAAGA

b        K L Y G S E G A D L L D G G E G N D L L -  
 481 -----+-----+-----+-----+-----+ 540  
       GAAAGGTGGATATGGTAATGATATTTATCGTTATCTTTCAGGATATGGCCATCATATTAT  
       CTTTCACCTATACCATTACTATAAATAGCAATAGAAAGTCTATACGGGTAGTATAATA

b        K G G Y G N D I Y R Y L S G Y G H H I I -  
 541 -----+-----+-----+-----+-----+ 600  
       TGACGATGAAGGGGGGAAAGACGATAAACTCAGTTTAGCTGATATAGATTTCCGGGACGT  
       ACTGCTACTTCCCCCTTTCTGCTATTTGAGTCAAATCGACTATATCTAAAGGCCCTGCA

b        D D E G G K D D K L S L A D I D F R D V -  
 601 -----+-----+-----+-----+-----+ 660  
       TGCCTTTAAGCGAGAAGGGAATGACCTCATTATGTATAAAGCTGAAGGTAATGTTCTTTC  
       ACGGAAATTCGCTCTTCCCTTACTGGAGTAATACATATTTGACTTCCATTACAAGAAAG

b        A F K R E G N D L I M Y K A E G N V L S -  
 661 -----+-----+-----+-----+-----+ 720  
       TATTGGCCACAAAAATGGTATTACATTAAAAACTGGTTTGAAAAAGAGTCAGATGATCT  
       ATAACCGGTGTTTTTACCATAATGTAAATTTTGGACAACTTTTTCTCAGTCTACTAGA

b        I G H K N G I T F K N W F E K E S D D L -  
 721 -----+-----+-----+-----+-----+ 780  
       CTCTAATCATCAGATAGAGCAGATTTTGTATAAAGACGGCAGGGTAATCACACCAGATTC  
       GAGATTAGTAGTCTATCTCGTCTAAAACTATTTCTGCCGTCCCATAGTGTGGTCTAAG

b        S N H Q I E Q I F D K D G R V I T P D S -  
 781 -----+-----+-----+-----+-----+ 840  
       TCTTAAAAAGCATTGGAATATCAGCAGAGTAATAACAAGGTAAGTTATGTGTATGGACA  
       AGAATTTTTTCGTAACTTATAGTCGTCTCATTATTGTTCCATTCAATACACATACCTGT

Fig. 7 (cont.)

b L K K A F E Y Q Q S N N K V S Y V Y G H -  
 841 TGATGCATCAACTTATGGGAGCCAGGACAATCTTAATCCATTAATTAATGAAATCAGCAA  
 -----+-----+-----+-----+-----+ 900  
 ACTACGTAGTTGAATACCCTCGGTCCTGTTAGAATTAGGTAATTAATTACTTTAGTCGTT

b D A S T Y G S Q D N L N P L I N E I S K -  
 BglII  
 |  
 901 AATCATTTCAGCTGCAGGTAACCTTCGATGTTAAGGAGGAAAGATCTGCCGCTTCTTTATT  
 -----+-----+-----+-----+-----+ 960  
 TTAGTAAAGTCGACGTCCATTGAAGCTACAATTCCTCCTTTCTAGACGGCGAAGAAATAA

b I I S A A G N F D V K E E R S A A S L L -  
 961 GCAGTTGTCCGTAATGCCAGTGATTTTTCATATGGACGGAACCTCAATAACTTTGACAGC  
 -----+-----+-----+-----+-----+ 1020  
 CGTCAACAGGCCATTACGCTCACTAAAAAGTATACCTGCCTTGAGTTATTGAAACTGTCTG

b Q L S G N A S D F S Y G R N S I T L T A -  
 1021 ATCAGCATAATATATTAATTTAAATGATAGCAATCTTACTGGGCTGTGCCACATAAGATT  
 -----+-----+-----+-----+-----+ 1080  
 TAGTCGTATTATATAATTAAATTTACTATCGTTAGAATGACCCGACACGGTGTATTCTAA

b S A \* -  
 1081 GCTATTTTTTTGGAGTCATAATGGATTCTTGTCAAAAATTGATTATGGGTATACGCCC  
 -----+-----+-----+-----+-----+ 1140  
 CGATAAAAAAACCTCAGTATTACCTAAGAACAGTATTTTAACTAATACCCAATATGCGGG

1141 TGGAGATTTTAGCCCAATACCATAACGTCTCTGTTAACCCGGAAGAAATTAAACATAGAT  
 -----+-----+-----+-----+-----+ 1200  
 ACCTCTAAATCGGGTTATGGTATTGCAGAGACAATTGGGCCTTCTTTAATTTGTATCTA

1201 TTGACACAGACGGGACTGGTCTGGGATTAACGTCATGGTTGCTTGCTGCGAAATCTTTAG  
 -----+-----+-----+-----+-----+ 1260  
 AACTGTGTCTGCCCTGACCAGACCCTAATTGCAGTACCAACGAACGACGCTTTAGAAATC

1261 AACTAAAGGTAAACAGGTAAAAAAACAATTGACCGATTAAACTTTATTTCTCTGCCCG  
 -----+-----+-----+-----+-----+ 1320  
 TTGATTTCCATTTTGTCCATTTTTTTTGTAACTGGCTAATTTGAAATAAAGAGACGGGC

1321 CATTAAGTCTGGAGAGAGGATGGACGTCATTTTATTCTGACTAAAGTCAGTAAAGAAGCAA  
 -----+-----+-----+-----+-----+ 1380  
 GTAATCAGACCTCTCTCCTACCTGCAGTAAAATAAGACTGATTTTCAGTCATTTCTTCGTT

Fig. 7 (cont.)

```

ACAGATATCTTATTTCTGATCTGGAGCAGCGAAATCCCGTGTTCTCGAACAGTCTGAGT
1381 -----+-----+-----+-----+-----+ 1440
TGTCCTATAGAATAAAGACTAGACCTCGTCGCTTTAGGGGCACAAGAGCTTGTCAGACTCA

TTGAGGCGTTATATCAGGGGCATATTATTCTTATCGCTTCCCGTTCTTCTGTTGCCGGGA
1441 -----+-----+-----+-----+-----+ 1500
AACTCCGCAATATAGTCCCGGTATAATAAGAATAGCGAAGGGCAAGAAGACAACGGCCCT

AACTGGCGAAATTTGACTTTACCTGGTTTATTCCTGCCATTATAAAATACAGGAGAATAT
1501 -----+-----+-----+-----+-----+ 1560
TTGACCGCTTTAAACTGAAATGGACCAAATAAGGACGTAATATTTTATGTCCTCTTATA

TTATTGAAACCCTTGTTGTGTCTGTTTTTTTACAATTATTTGCATTAATAACCCCTTTT
1561 -----+-----+-----+-----+-----+ 1620
AATAACTTTGGGAACAACACAGACAAAAAATGTTAATAAACGTAATTATTGGGGGGAAA

TTTTTCAGGTGGTTATGGACAAAGTATTAGTGCACAGGGGATTTTCAACTCTTAATGTTA
1621 -----+-----+-----+-----+-----+ 1680
AAAAAGTCCACCAATACCTGTTTCATAATCACGTGTCCCTAAAAGTTGAGAATTACAAT

TTACTGTGCGATTATCTGTTGTGGTGGTGGTTGAGATTATACTCAGCGGTTTAAGAACTT
1681 -----+-----+-----+-----+-----+ 1740
AATGACAGCGTAATAGACAACACCACCACAACTCTAATATGAGTCGCCAAATCTTGAA

ACATTTTTGCACATAGTACAAGTCGGATTGATGTTGAGTTGGGTGCCAAACTCTTCCGGC
1741 -----+-----+-----+-----+-----+ 1800
TGTA AAAACGTGTATCATGTT CAGCCTAACTACA ACTCAACCCACGGTTTGAGAAGGCCG

ATTACTGGCGCTACCGATCTCTTATTTTGAGAGTCGTCGTGTTGGTGATACTGTTGCCA
1801 -----+-----+-----+-----+-----+ 1860
TAAATGACCGCGATGGCTAGAGAATAAACTCTCAGCAGCACAACTATGACAACGGT

GGGTAAGAGAATTAGACCAGATCCGTAATTTTCTGACAGGACAGGCATTAACATCTGTTCT
1861 -----+-----+-----+-----+-----+ 1920
CCCATTCTCTTAATCTGGTCTAGGCATTAAAGACTGTCCTGTCCGTAATTGTAGACAAG

                                     HindIII
                                     |
TGGACTTATTATTTTCATTCATATTTTGTGCGGTAATGTGGTATTACAGTCCAAAGCTT
1921 -----+-----+-----+-----+-----+ 1979
ACCTGAATAATAAAAGTAAGTATAAAAAACGCCATTACACCATAATGTCAGGTTTCGAA

```

Fig. 7 (cont.)



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Cutting enzymes:

BamHI	BglII	EagI	EcoRI	HindIII	NcoI	NheI	SalI
SfiI	XbaI	XmaI					

Not cutting enzymes:

None

Fig. 7 (cont.)

pVamyHLYA map

With 8 enzymes: NCOI PSTI SALI HINDIII SFII BAMHI NOTI ECORI PSTI

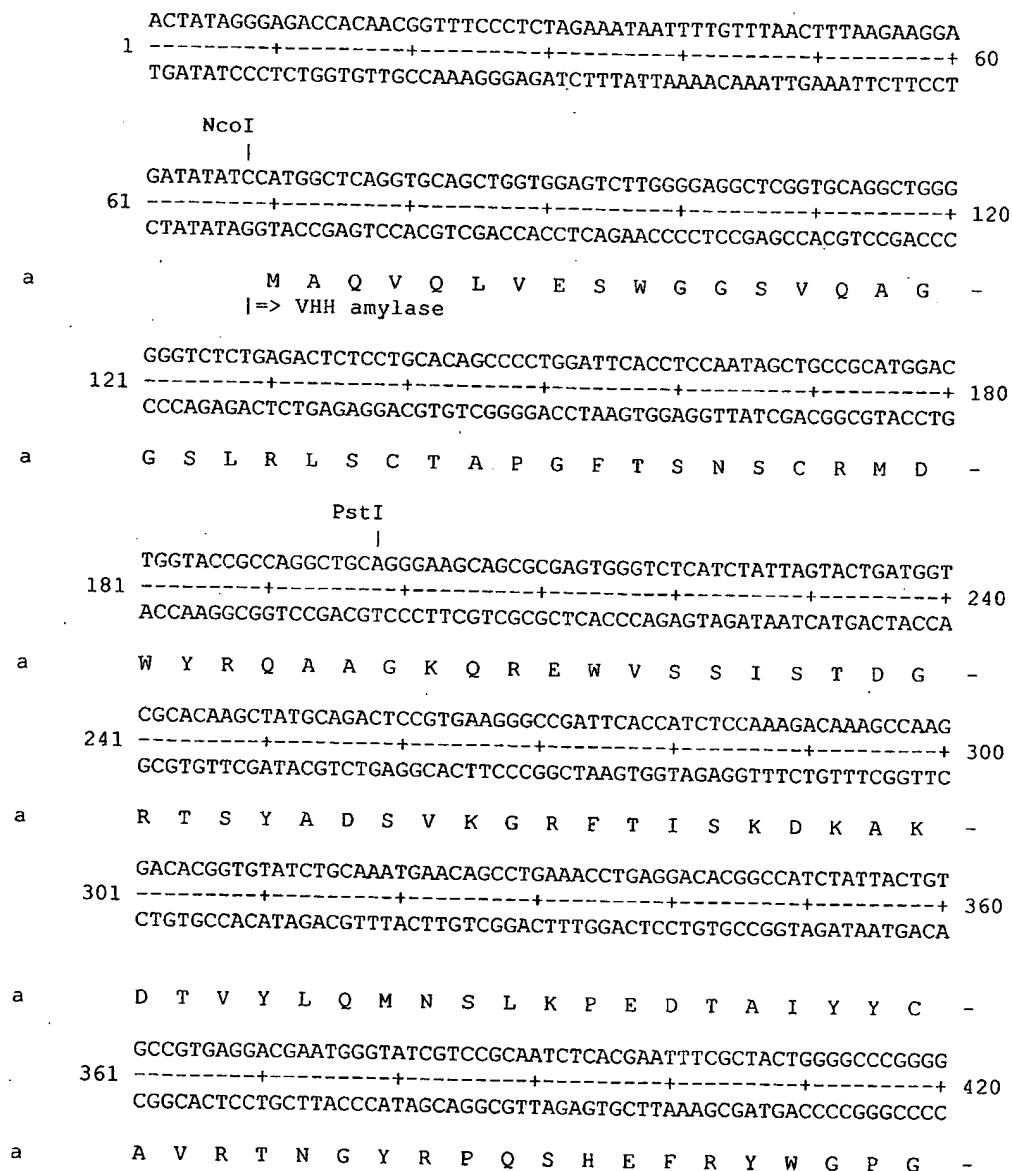


Fig. 8

Fig. 8 (cont.)

```

a      R V I T P D S L K K A F E Y Q Q S N N K -
      GTAAGTTATGTGTATGGACATGATGCATCAACTTATGGGAGCCAGGACAATCTTAATCCA
961  -----+-----+-----+-----+-----+-----+-----+ 1020
      CATTCAATACACATACCTGTACTACGTAGTTGAATACCCTCGGTCCTGTTAGAATTAGGT

a      V S Y V Y G H D A S T Y G S Q D N L N P -
                                PstI
                                |
      TTAATTAATGAAATCAGCAAAATCATTTCAGCTGCAGGTAACCTTCGATGTTAAGGAGGAA
1021  -----+-----+-----+-----+-----+-----+-----+ 1080
      AATTAATTACTTTAGTCGTTTTAGTAAAGTCGACGTCCATTGAAGCTACAATTCCTCCTT

a      L I N E I S K I I S A A G N F D V K E E -
      AGATCTGCCGCTTCTTTATTGCAGTTGTCCGGTAATGCCAGTGATTTTTTCATATGGACGG
1081  -----+-----+-----+-----+-----+-----+-----+ 1140
      TCTAGACGGCGAAGAAATAACGTCAACAGGCCATTACGGTCACTAAAAAGTATACCTGCC

a      R S A A S L L Q L S G N A S D F S Y G R -
      AACTCAATAACTTTGACAGCATCAGCATAATATATTAATTTAAATGATAGCAATCTTACT
1141  -----+-----+-----+-----+-----+-----+-----+ 1200
      TTGAGTTATTGAAACTGTCGTAGTCGTATTATATAATTAATTTACTATCGTTAGAATGA

a      N S I T L T A S A * -
      GGGCTGTGCCACATAAGATTGCTATTTTTTTGGAGTCATAATGGATTCTTGTCATAAAAT
1201  -----+-----+-----+-----+-----+-----+-----+ 1260
      CCCGACACGGTGTATTCTAACGATAAAAAAACCTCAGTATTACCTAAGAACAGTATTTTA

      TGATTATGGGTTATACGCCCTGGAGATTTAGCCCAATACCATAACGTCTCTGTTAACCC
1261  -----+-----+-----+-----+-----+-----+-----+ 1320
      ACTAATACCCAATATGCGGGACCTCTAAATCGGGTTATGGTATTGCAGAGACAATTGGG

      GGAAGAAATTAAACATAGATTTGACACAGACGGGACTGGTCTGGGATTAACGTCATGGTT
1321  -----+-----+-----+-----+-----+-----+-----+ 1380
      CCTTCTTTAATTTGTATCTAAACTGTGTCTGCCCTGACCAGACCCTAATTGCAGTACCAA

      GCTTGCTGCGAAATCTTTAGAACTAAAGGTAAACAGGTAAAAAAACAATTGACCGATT
1381  -----+-----+-----+-----+-----+-----+-----+ 1440
      CGAACGACGCTTTAGAAATCTTGATTCCATTTTGTCCATTTTTTTTGTAACTGGCTAA

      AAACTTTATTTCTCTGCCCGCATTAGTCTGGAGAGAGGATGGACGTCATTTTATTCTGAC
1441  -----+-----+-----+-----+-----+-----+-----+ 1500
      TTTGAAATAAAGAGACGGGCGTAATCAGACCTCTCTCCTACCTGCAGTAAATAAGACTG

```

Fig. 8 (cont.)

```

TAAAGTCAGTAAAGAAGCAAACAGATATCTTATTTCTGATCTGGAGCAGCGAAATCCCCG
1501 -----+-----+-----+-----+-----+ 1560
ATTTTCAGTCATTTCTTCGTTTGTCTATAGAATAAAGACTAGACCTCGTCGCTTTAGGGGC

TGTTCCTCGAACAGTCTGAGTTTGAGGCGTTATATCAGGGGCATATTATTCTTATCGCTTC
1561 -----+-----+-----+-----+-----+ 1620
ACAAGAGCTTGTCTAGACTCAAACCTCCGCAATATAGTCCCGGTATAATAAGAATAGCGAAG

CCGTTCTTCTGTGTCGGGAAACTGGCGAAATTTGACTTTACCTGGTTTATTCTGCCAT
1621 -----+-----+-----+-----+-----+ 1680
GGCAAGAAGACAACGGCCCTTTGACCGCTTTAAACTGAAATGGACCAAATAAGGACGGTA

TATAAAATACAGGAGAATATTTATTGAAACCTTGTTGTCTGTGTTTTTTTACAATTATT
1681 -----+-----+-----+-----+-----+ 1740
ATATTTTATGTCCTCTTATAAATAACTTTGGGAACAACACAGACAAAAAATGTTAATAA

TGCATTAATAACCCCCCTTTTTTTTCAGGTGGTTATGGACAAAGTATTAGTGCACAGGGG
1741 -----+-----+-----+-----+-----+ 1800
ACGTAATTATTGGGGGAAAAAAGTCCACCAATACCTGTTTCATAATCACGTGTCCCC

ATTTTCAACTCTTAATGTTATTACTGTCTGATTATCTGTTGTGGTGGTGGTTGAGATTAT
1801 -----+-----+-----+-----+-----+ 1860
TAAAGTTGAGAATTACAATAATGACAGCGTAATAGACAACACCACCACAACTCTAATA

ACTCAGCGGTTTAAGAACTTACATTTTGCACATAGTACAAGTCGGATTGATGTTGAGTT
1861 -----+-----+-----+-----+-----+ 1920
TGAGTCGCCAAATTCTTGAATGTAAAACGTGTATCATGTTTCAGCCTAACTACAAC TCA

GGGTGCCAAACTCTTCCGGCATTACTGGCGCTACCGATCTCTTATTTTGAGAGTCGTCG
1921 -----+-----+-----+-----+-----+ 1980
CCCACGGTTTGAGAAGGCGTAATGACCGCGATGGCTAGAGAATAAACTCTCAGCAGC

TGTTGGTGATACTGTTGCCAGGGTAAGAGAATTAGACCAGATCCGTAATTTTCTGACAGG
1981 -----+-----+-----+-----+-----+ 2040
ACAACCACTATGACAACGGTCCCATTTCTTAACTCTGGTCTAGGCATTTAAAGACTGTCC

ACAGGCATTAACATCTGTTCTGGACTTATTATTTTCATTCATATTTTTTGCGGTAATGTG
2041 -----+-----+-----+-----+-----+ 2100
TGTCCGTAATTGTAGACAAGACCTGAATAATAAAGTAAGTATAAAAAACGCCATTACAC

```

Fig. 8 (cont.)

HindIII  
|

2101 GTATTACAGTCCAAAGCTTACTCTGGTGATCTTATTTTCGCTGCCTTGTTATGCTGCATG  
-----+-----+-----+-----+-----+-----+ 2160  
CATAATGTCAGGTTTCGAATGAGACCACTAGAAATAAAGCGACGGAACAATACGACGTAC

2161 GTCTGTTTTATTAGCCCCATTTTGGCAGCTCGCCTTGATGATAAGTTTTACGGAATGC  
-----+-----+-----+-----+-----+-----+ 2220  
CAGACAAAATAATCGGGTAAAACGCTGCAGCGGAACACTATTCAAAGTGCCTTACG

2221 GGATAATCAATCTTTCCTGGTGAATCAGTCACGGCGATTAACTATAAAAGCTATGGC  
-----+-----+-----+-----+-----+-----+ 2280  
CCTATTAGTTAGAAAGGACCACCTTAGTCAGTGCCGCTAATTGTGATATTTTCGATACCG

PstI  
|

2281 AGTCTCACCTCAGATGACGAACATATGGGACAAACAATTGGCAGGATATGTTGCTGCAGG  
-----+-----+-----+-----+-----+-----+ 2340  
TCAGAGTGGAGTCTACTGCTTGATACCCTGTTGTTAACCGTCTATACAACGACGTCC

2341 CTTCAAAGTGACAGTATTAGCAACCATTGGTCAACAAGGAATACAGTTAATAACAAAAGAC  
-----+-----+-----+-----+-----+-----+ 2400  
GAAGTTTCACTGTCATAATCGTTGGTAACCAAGTTGTTCTTATGTCAATTATGTTTCTG

2401 TGTTATGATCATCAACCTGTGGTTGGGAGCACACCTGGTTATTTCCGGGGATTAAAGTAT  
-----+-----+-----+-----+-----+-----+ 2460  
ACAATACTAGTAGTTGGACACCAACCCTCGTGTGGACCAATAAGGCCCTAAATTCATA

2461 TGGTCAGTTAATTGCTTTTAATATGCTTGCTGGTCAGATTGTTGCACCGGTTATTTCGCCT  
-----+-----+-----+-----+-----+-----+ 2520  
ACCACTCAATTAACGAAAATTATACGAACGACCAAGTCTAACAACGTGGCCAATAAGCGGA

2521 TGCACAAATCTGGCAGGATTTCCAGCAGGTTGGTATATCAGTTACCCGCCTTGGTGATGT  
-----+-----+-----+-----+-----+-----+ 2580  
ACGTGTTTAGACCGTCTAAAGGTCTGTCACCAACATATAGTCAATGGCGGAACCACTACA

2581 GCTTAACTCTCCTGAAAGTTATCATGGGAACTGGCATTACCGGAAATTAATGGTGA  
-----+-----+-----+-----+-----+-----+ 2640  
CGAATTGAGAGGTTGACTTTCAATAGTACCCTTTGACCGTAATGGCCTTTAATTACCACT

2641 TATCACTTTTCGTAATATCCGGTTTCGCTATAAGCCTGACTCTCCGGTTATTTAGATAA  
-----+-----+-----+-----+-----+-----+ 2700  
ATAGTGAAGCAATTATAGGCCAAAGCGATATTCGGACTGAGAGGCCAATAAATCTATT

2701 TATCAATCTCAGTATTAAGCAGGGGGAGGTTATTGGTATTGTGCGACGTTCTGGTTCAGG  
-----+-----+-----+-----+-----+-----+ 2760  
ATAGTTAGAGTCATAATTCGTCCCCCTCCAATAACCATAACAGCCTGCAAGACCAAGTCC

Fig. 8 (cont.)

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2761 AAAAAGCACATTAACATAAATTAATTCAACGTT 2792  
-----+-----+-----+-----  
TTTTTCGTGTAATTGATTTAATTAAGTTGCAA

Cutting enzymes:

BamHI HindIII NcoI PstI SalI SfiI

Not cutting enzymes:

EcoRI NotI

Fig. 8 (cont.)

PVamyZHLA map

With 11 enzymes: ECORI SPHI PSTI NCOI NHEI NDEI BAMHI HINDIII  
SALI SFII NOTI

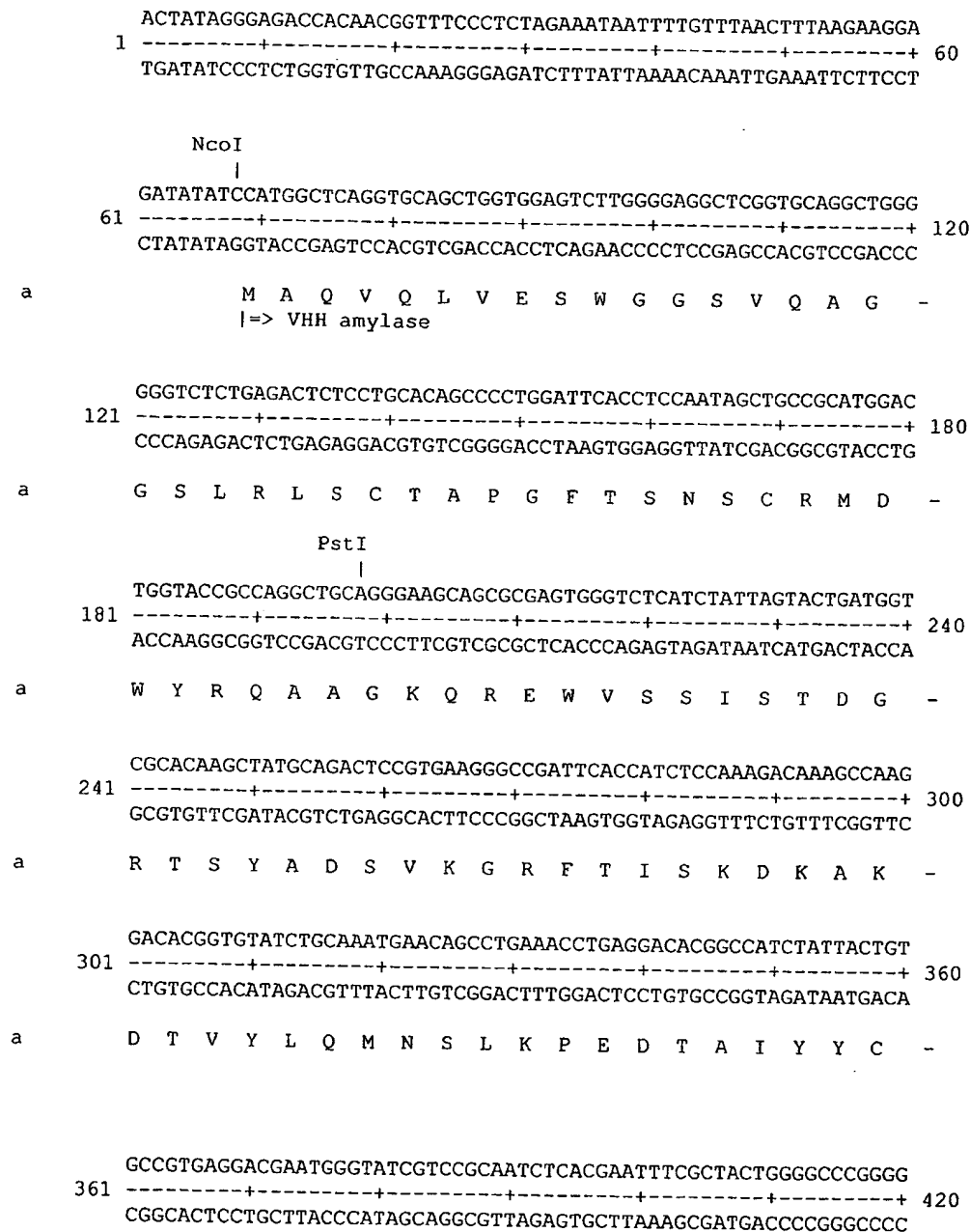


Fig. 9



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```

a      A V R T N G Y R P Q S H E F R Y W G P G -

                                SfiI   SalI
                                |       |
                                +       +
421  ACCCAGGTCACCGTCTCCTCAACGGCCTCGGGGGCCGCGTCGACGTCCGGCGGTCCGAAG
-----+-----+-----+-----+-----+-----+-----+-----+
TGGGTCCAGTGGCAGAGGAGTTGCCGGAGCCCCCGGCGCAGCTGCAGGCCGCCAGGCTTC
                                +-----+-----+-----+-----+-----+
a      T Q V T V S S T A S G A A S T S G G P K -
                                           |=> Ig hinge

CCTTCCACTCCGCCCCGGGTCTTCCCGTATGAAACAGCTGGAAGACAAAGTAGAgGAGCTC
481  -----+-----+-----+-----+-----+-----+-----+
GGAAGGTGAGGCGGGCCCAGAAGGGCATACTTTGTCGACCTTCTGTTTCATCTTCTCGAG

a      P S T P P G S S R M K Q L E D K V E E L -
                                |=> Leucine Zipper GCN4

                                HindIII
                                |
                                +-----+-----+-----+-----+-----+
541  CTTAGCAAGAACTACCATCTAGAAAACGAGGTAGCTCGTCTGAAAAAGCTTGTGGTGAA
-----+-----+-----+-----+-----+-----+-----+
GAATCGTTCTTGATGGTAGATCTTTTGCTCCATCGAGCAGACTTTTTCGAACAACCACTT

a      L S K N Y H L E N E V A R L K K L V G E -

                                SalI
                                |
                                +-----+-----+-----+-----+-----+
601  CGTGGTGGTCACCATCACCATCACCATGCGTCGACGCCCGGGGGTGCGCCGGTGCCGTAT
-----+-----+-----+-----+-----+-----+-----+
GCACCACCACTGGTAGTGGTAGGTACGCAGCTGCGGGCCCCACGCGGCCACGGCATA

a      R G G H H H H H A S T P G G A P V P Y -
                                |=> 6xhis tag                                |=> E-tag

BamHI
|
+-----+-----+-----+-----+-----+-----+-----+
661  CCGGATCCGCTGGAACCGGCCGGGgAAAATtCTCTTGCTAAAAATGTATTATCCGGTGA
-----+-----+-----+-----+-----+-----+-----+
GGCCTAGGCGACCTTGGCCGGCCCCtTTTAAgAGAACGATTTTACATAATAGGCCACCT

a      P D P L E P A G E N S L A K N V L S G G -
                                |=> C-hlyA

AAAGGTAATGACAAGTTGTACGGCAGTGAGGGAGCAGACCTGCTTGATGGCGGAGAAGGG
721  -----+-----+-----+-----+-----+-----+-----+
TTTCATTACTGTTCAACATGCCGTCACTCCCTCGTCTGGACGAACTACCGCCTCTTCCC

a      K G N D K L Y G S E G A D L L D G G E G -

```

Fig. 9 (cont.)

```

AATGATCTTCTGAAAGGTGGATATGGTAATGATATTATCGTTATCTTTCAGGATATGGC
781 -----+-----+-----+-----+-----+-----+-----+-----+ 840
TTACTAGAAGACTTTCCACCTATACCATTACTATAAATAGCAATAGAAAGTCCTATACCG

a      N D L L K G G Y G N D I Y R Y L S G Y G -

CATCATATTATTGACGATGAAGGGGGGAAAGACGATAAACTCAGTTTAGCTGATATAGAT
841 -----+-----+-----+-----+-----+-----+-----+ 900
GTAGTATAATAACTGCTACTTCCCCCTTTCTGCTATTTGAGTCAAATCGACTATATCTA

a      H H I I D D E G G K D D K L S L A D I D -

TTCCGGGACGTTGCCTTTAAGCGAGAAGGGAATGACCTCATTATGTATAAAGCTGAAGGT
901 -----+-----+-----+-----+-----+-----+-----+ 960
AAGGCCCTGCAACGGAATTGCTCTTCCCTTACTGGAGTAATACATATTTGACTTCCA

a      F R D V A F K R E G N D L I M Y K A E G -

AATGTTCTTTCTATTGGCCACAAAATGGTATTACATTTAAAACTGGTTTGAAAAAGAG
961 -----+-----+-----+-----+-----+-----+-----+ 1020
TTACAAGAAAGATAACCGGTGTTTTTACCATAATGTAAATTTTACCAAACCTTTTCTC

a      N V L S I G H K N G I T F K N W F E K E -

TCAGATGATCTCTCTAATCATCAGATAGAGCAGATTTTGTATAAAGACGGCAGGGTAATC
1021 -----+-----+-----+-----+-----+-----+-----+ 1080
AGTCTACTAGAGAGATTAGTAGTCTATCTCGTCTAAAACTATTTCTGCCGTCCCATTAG

a      S D D L S N H Q I E Q I F D K D G R V I -

ACACCAGATTCTCTTAAAAAGCATTGGAATATCAGCAGAGTAATAACAAGGTAAGTTAT
1081 -----+-----+-----+-----+-----+-----+-----+ 1140
TGTGGTCTAAGAGAATTTTTTCGTAACTTATAGTCGTCTCATTATTGTTCCATTCAATA

a      T P D S L K K A F E Y Q Q S N N K V S Y -

GTGTATGGACATGATGCATCAACTTATGGGAGCCAGGACAATCTTAATCCATTAATTAAT
1141 -----+-----+-----+-----+-----+-----+-----+ 1200
CACATACCTGTACTACGTAGTTGAATACCTCGGTCCTGTTAGAATTAGGTAATTAATTA

a      V Y G H D A S T Y G S Q D N L N P L I N -

```

Fig. 9 (cont.)

PstI

```

      |
GAAATCAGCAAAATCATTTCAGCTGCAGGTAACCTCGATGTTAAGGAGGAAAGATCTGCC
1201 -----+-----+-----+-----+-----+-----+ 1260
      CTTTAGTCGTTTTAGTAAAGTCGACGTCCATTGAAGCTACAATTCCTTCTAGACGG
a      E I S K I I S A A G N F D V K E E R S A -

      NdeI
      |
GCTTCTTTATTGCAGTTGTCCGTAATGCCAGTGATTTTTCATATGGACGGAACCTCAATA
1261 -----+-----+-----+-----+-----+ 1320
      CGAAGAAATAACGTCAACAGGCCATTACGGTCACTAAAAAGTATACCTGCCTTGAGTTAT
a      A S L L Q L S G N A S D F S Y G R N S I -

      ACTTTGACAGCATCAGCATAATATATTAATTAAATGATAGCAATCTTACTGGGCTGTGC
1321 -----+-----+-----+-----+-----+ 1380
      TGAACTGTCGTAGTCGTATTATATAATTAATTTACTATCGTTAGAATGACCCGACACG
a      T L T A S A * -

      CACATAAGATTGCTATTTTTTTGGAGTCATAATGGATTCTTGTCATAAAATTGATTATGG
1381 -----+-----+-----+-----+-----+ 1440
      GTGTATTCTAACGATAAAAAAACCTCAGTATTACCTAAGAACAGTATTTTAACTAATACC

      GTTATACGCCCTGGAGATTTTAGCCCAATACCATAACGTCTCTGTAAACCCGGAAGAAAT
1441 -----+-----+-----+-----+-----+ 1500
      CAATATGCGGGACCTCTAAATCGGGTTATGGTATTGCAGAGACAATTGGGCCTTCTTTA

      TAAACATAGATTTGACACAGACGGGACTGGTCTGGGATTAACGTCATGGTTGCTTGCTGC
1501 -----+-----+-----+-----+-----+ 1560
      ATTTGTATCTAAACTGTGCTGCCCTGACCAGACCTAATTGCAGTACCAACGAACGACG

      GAAATCTTTAGAACTAAAGGTAAAACAGGTAAAAAAAACAATTGACCGATTAACTTTAT
1561 -----+-----+-----+-----+-----+ 1620
      CTTTAGAAATCTTGATTCCATTTTGTCCATTTTTTTTGTAACTGGCTAATTGAAATA

      TTCTCTGCCCGCATTAGTCTGGAGAGAGGATGGACGTCATTTTATTCTGACTAAAGTCAG
1621 -----+-----+-----+-----+-----+ 1680
      AAGAGACGGGCGTAATCAGACCTCTCTCCTACCTGCAGTAAAATAAGACTGATTTTCAGTC

      TAAAGAAGCAAACAGATATCTTATTTCTGATCTGGAGCAGCGAAATCCCGTGTTCTCGA
1681 -----+-----+-----+-----+-----+ 1740
      ATTTCTTCGTTTGTCTATAGAATAAAGACTAGACCTCGTCGCTTTAGGGGCACAAGAGCT

```

Fig. 9 (cont.)

```

ACAGTCTGAGTTTGAGGCGTTATATCAGGGGCATATTATTCTTATCGCTTCCC GTTCTTC
1741 -----+-----+-----+-----+-----+-----+ 1800
TGTCAGACTCAAACCTCCGCAATATAGTCCCCGTATAATAAGAATAGCGAAGGGCAAGAAG

TGTTGCCGGGAAACTGGCGAAATTTGACTTTACCTGGTTTATTCCTGCCATTATAAAATA
1801 -----+-----+-----+-----+-----+-----+ 1860
ACAACGGCCCTTTGACCGCTTTAAACTGAAATGGACCAAATAAGGACGGTAATATTTTAT

CAGGAGAATATTTATTGAAACCCCTTGTGTGTCTGTTTTTTTACAATTATTTGCATTAAT
1861 -----+-----+-----+-----+-----+-----+ 1920
GTCCTCTTATAATAACTTTGGGAACAACACAGACAAAAAATGTTAATAAACGTAATTA

AACCCCCCTTTTTTTTCAGGTGGTTATGGACAAAGTATTAGTGCACAGGGGATTTTCAAC
1921 -----+-----+-----+-----+-----+-----+ 1980
TTGGGGGGAAAAAAGTCCACCAATACCTGTTTCATAATCACGTGTCCCCTAAAAGTTG

TCTTAATGTTATTACTGTGCGATTATCTGTTGTGGTGGTGTGTTGAGATTATACTCAGCGG
1981 -----+-----+-----+-----+-----+-----+ 2040
AGAATTACAATAATGACAGCGTAATAGACAACACCACCACAAACTCTAATATGAGTCGCC

TTTAAGAACTTACATTTTTGCACATAGTACAAGTCGGATTGATGTTGAGTTGGGTGCCAA
2041 -----+-----+-----+-----+-----+-----+ 2100
AAATTCTTGAATGTAAAACGTGTATCATGTTTCAGCCTAACTACAACCTCAACCCACGGTT

ACTCTTCCGGCATTACTGGCGCTACCGATCTCTTATTTTGAGAGTCGTCGTGTTGGTGA
2101 -----+-----+-----+-----+-----+-----+ 2160
TGAGAAGGCCGTAAATGACCGCGATGGCTAGAGAATAAAACTCTCAGCAGCACAACTACT

TACTGTTGCCAGGGTAAGAGAATTAGACCAGATCCGTAATTTTCTGACAGGACAGGCATT
2161 -----+-----+-----+-----+-----+-----+ 2220
ATGACAACGGTCCCATTCTCTTAATCTGGTCTAGGCATTAAAAGACTGTCCTGTCCGTAA

AACATCTGTTCTGGACTTATTATTTTCATTCATATTTTTTGCGGTAATGTGGTATTACAG
2221 -----+-----+-----+-----+-----+-----+ 2280
TTGTAGACAAGACCTGAATAATAAAAGTAAGTATAAAAAACGCCATTACACCATAATGTC

HindIII
|
TCCAAAGCTTACTCTGGTGATCTTATTTTCGCTGCCTTGTTATGCTGCATGGTCTGTTTT
2281 -----+-----+-----+-----+-----+-----+ 2340
AGGTTTCGAATGAGACCACTAGAATAAAAGCGACGGAACAATACGACGTACCAGACAAA

TATTAGCCCCATTTTGGCAGCTCGCCTTGATGATAAGTTTTTCACGGAATGCGGATAATCA
2341 -----+-----+-----+-----+-----+-----+ 2400
ATAATCGGGGTAAAACGCTGCAGCGGAACACTATTCAAAGTGCCTTACGCCTATTAGT

```

Fig. 9 (cont.)

```

ATCTTTCCTGGTGAATCAGTCACGGCGATTAACACTATAAAAGCTATGGCAGTCTCACC
2401 -----+-----+-----+-----+-----+-----+ 2460
TAGAAAGGACCACCTTAGTCAGTGCCGCTAATTGTGATATTTTCGATACCGTCAGAGTGG

                NdeI                               PstI
                |                                   |
TCAGATGACGAACATATGGGACAAACAATTGGCAGGATATGTTGCTGCAGGCTTCAAAGT
2461 -----+-----+-----+-----+-----+-----+ 2520
AGTCTACTGCTTGTATACCTGTTTGTAAACCGTCTATACAACGACGTCCGAAGTTTCA

GACAGTATTAGCAACCATTGGTCAACAAGGAATACAGTTAATACAAAAGACTGTTATGAT
2521 -----+-----+-----+-----+-----+-----+ 2580
CTGTCATAATCGTTGGTAACCAAGTTGTTCCCTATGTCAATTATGTTTCTGACAATACTA

CATCAACCTGTGGTGGGAGCACACCTGGTTATTTCCGGGGATTAAAGTATTGGTCAGTT
2581 -----+-----+-----+-----+-----+-----+ 2640
GTAGTTGGACACCAACCCTCGTGTGGACCAATAAAGGCCCTAAATTCATAACCAGTCAA

AATTGCTTTTAATATGCTTGCTGGTCAGATTGTTGCACCGGTTATTCGCCTTGCACAAAT
2641 -----+-----+-----+-----+-----+-----+ 2700
TTAACGAAAATTATACGAACGACCAGTCTAACAACGTGGCCAATAAGCGGAACGTGTTA

CTGGCAGGATTTCCAGCAGGTTGGTATATCAGTTACCCGCCTTGGTGATGTGCTTAACTC
2701 -----+-----+-----+-----+-----+-----+ 2760
GACCGTCTAAAGGTCGTCCAACCATATAGTCAATGGGCGGAACCACTACACGAATTGAG

TCCAACTGAAAGTTATCATGGGAAACTGGCATTACCGGAAATTAATGGTGATATCACTTT
2761 -----+-----+-----+-----+-----+-----+ 2820
AGGTTGACTTTCAATAGTACCCTTTGACCGTAATGGCCTTTAATTACCACTATAGTGAAA

TCGTAATATCCGGTTTCGCTATAAGCCTGACTCTCCGGTTATTTTAGATAATATCAATCT
2821 -----+-----+-----+-----+-----+-----+ 2880
AGCATTATAGGCCAAAGCGATATTCGGACTGAGAGGCCAATAAAATCTATTATAGTTAGA

CAGTATTAAGCAGGGGGAGGTTATTGGTATTGTGCGACGTTCTGGTTCAGGAAAAAGCAC
2881 -----+-----+-----+-----+-----+-----+ 2940
GTCATAATTGTCCTCCCTCCAATAACCATAACAGCCTGCAAGACCAAGTCCTTTTCGTG

ATTAACATAAATTAATTCAACGTT
2941 -----+-----+-----+-----+-----+ 2963
TAATTGATTTAATTAAGTTGCAA

```

Fig. 9 (cont.)

30/30

Cutting enzymes:

BamHI	HindIII	NcoI	NdeI	PstI	SalI	SfiI
-------	---------	------	------	------	------	------

Not cutting enzymes:

EcoRI	NheI	NotI	SphI
-------	------	------	------

**Fig. 9 (cont.)**

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